

# 4

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/831,656

DATE: 09/27/2001  
TIME: 11:59:29

Input Set : A:\5753prj.ST25.txt  
Output Set: N:\CRF3\09272001\I831656.raw

3 <110> APPLICANT: Novozymes A/S  
 4 Nielsen, Jack Bech  
 5 Kjaerulff, Soren  
 7 <120> TITLE OF INVENTION: Transgenic Plant Expressing Maltogenic Alpha-Amylase  
 9 <130> FILE REFERENCE: 5753.204-US  
 11 <140> CURRENT APPLICATION NUMBER: 09/831,656  
 C--> 12 <141> CURRENT FILING DATE: 2001-08-23  
 14 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00624  
 15 <151> PRIOR FILING DATE: 1999-11-12  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2160  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Bacillus sp.  
 26 <400> SEQUENCE: 1

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29 agcggttctc ttccgtacaa tccaaacggcc gctgaagccca gcagttccgc aagcgtcaaa	120
31 ggggacgtga tttaccagat tatcatttgc acgttttacg atggggacac gacgaacaac	180
33 aatcctgcca aaagttagg actttacgat ccgaccaa at cgaagtggaa aatgtattgg	240
35 ggcggggatc tggagggggt tcgtcaaaaaa ctcccttatac ttaaacagct gggcgtaaacg	300
37 acaatctggt tgtccccgtt tttggacaat ctggatacac tggcgccgac cgataacacg	360
39 ggctatcagc gatactggac ggcgcattttt aaacagattt aggaacattt cggaaatttgg	420
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43 ttgtgcccata atcatttgc ac tccctttaag gcaaacgatt ccaccttgc ggaaggcgcc	540
45 gccctctaca acaatggAAC ctatatgggc aatttttg atgacgcaac aaaagggtac	600
47 ttccaccata atggggacat cagcaactgg gacgaccggc acgaggcgca atggaaaaac	660
49 ttacggatc cagccggttt ctgcgttgc gatttgcgc aggaaaatgg cacgattgct	720
51 caatacctga ccgtatcgcc ggttcaattt gtagcacatg gagcggatgg tttcggtt	780
53 gatgcgggtga agcatttaa ttccgggttc tccaaatcgt tggccgataa actgtaccaa	840
55 aagaaagaca ttttccgtt gggggatgg tacggagatg accccggaaac agccaatcat	900
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61 gtaacccaaa cggggAACGA gtacaaatac aaagaaaatc taatcacatt tatcgataac	1080
63 catgatatgt caagatttct ttccgttaat tgcgacaagg cgaatttgc ccagcgctt	1140
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71 ggcaccacca cccagcggtt gatcaacaat gatgtttaca tttatgaacg gaaatttttc	1380
73 aacgatgtcg tgggtggc catcaatcg aacacgcaat ctccttattt gattccgg	1440
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83 accgtgacat ttggcgaggat gacagcgact gtgaaatcct gacatccaa tcggattgaa	1740
85 gtgtacgttc ccaacatggc cgccggctg accgatgtga aagtcaccgc gggtgagtt	1800
87 tccagcaatc tgttatttca caatattttt gatggAACGC agacatcggt tggtttact	1860

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89	gtgaaaagtgcgcctccgac	caacctgggg	gataagattt	acctgacggg	caacataccg	1920
91	gaattggggat	ttggagcac	ggatacgagc	ggagccgtta	acaatgcgca	1980
93	ctcgcccca	attatccgga	ttggtttat	gtattcagcg	ttccagcagg	2040
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112	20	25	30			
115	Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile					
116	35	40	45			
119	Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys					
120	50	55	60			
123	Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp					
124	65	70	75	80		
127	Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln					
128	85	90	95			
131	Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp					
132	100	105	110			
135	Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg					
136	115	120	125			
139	Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp					
140	130	135	140			
143	Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp					
144	145	150	155	160		
147	Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe					
148	165	170	175			
151	Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr					
152	180	185	190			
155	Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser					
156	195	200	205			
159	Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro					
160	210	215	220			
163	Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala					
164	225	230	235	240		
167	Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp					
168	245	250	255			
171	Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys					
172	260	265	270			
175	Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly					
176	275	280	285			
179	Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val					
180	290	295	300			
183	Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn					

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184	305	310	315	320
187	Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp			
188	325	330	335	
191	Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu			
192	340	345	350	
195	Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser			
196	355	360	365	
199	Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu			
200	370	375	380	
203	Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met			
204	385	390	395	400
207	Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp			
208	405	410	415	
211	Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg			
212	420	425	430	
215	Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile			
216	435	440	445	
219	Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val			
220	450	455	460	
223	Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly			
224	465	470	475	480
227	Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly			
228	485	490	495	
231	Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser			
232	500	505	510	
235	Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser			
236	515	520	525	
239	Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro			
240	530	535	540	
243	Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly			
244	545	550	555	560
247	Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser			
248	565	570	575	
251	Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp			
252	580	585	590	
255	Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn			
256	595	600	605	
259	Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala			
260	610	615	620	
263	Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro			
264	625	630	635	640
267	Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala			
268	645	650	655	
271	Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe			
272	660	665	670	
275	Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg			
276	675	680	685	
279	Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr			
280	690	695	700	

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283 Thr Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn  
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289 <212> TYPE: DNA  
290 <213> ORGANISM: Artificial Sequence  
292 <220> FEATURE:  
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300 <211> LENGTH: 25  
301 <212> TYPE: DNA  
302 <213> ORGANISM: Artificial Sequence  
304 <220> FEATURE:  
305 <223> OTHER INFORMATION: RNP 110 ✓  
307 <400> SEQUENCE: 4  
308 cgatgagctc ctatgttgc cacgt

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date